Saskatchewan
Agriculture
and Food

ADF

AGRICULTURE DEVELOPMENT FUND

FINAL REPORT

20040522

DEVELOPMENT OF FOOD GRADE CANARYSEED

Funded by: The Agriculture Development Fund

January 2008

Prepared by: University of Saskatchewan (U of S)

ADF PROJECT 20040522

"DEVELOPMENT OF FOOD GRADE CANARY SEED"

Final Report

July 1, 2005 to December 31, 2007

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ABSTRACT

After three years of field evaluation it was possible to identify glabrous-yellow seeded (potential food-use canaryseed) lines that are equal in performance to glabrous brown seeded cultivars. The most promising lines yielded 11 to 19% higher than CDC Maria and 3 to 10% higher than CDC Togo. The growth regulator ethrel did not appear to be an effective gametocide in canaryseed due to incomplete male sterility. Canaryseed specific molecular markers which would have enabled high-through put screening and the ability to measure hybridity could not be isolated during the course of this study.

INTRODUCTION

Background Information

Canaryseed acreage in Saskatchewan has increased by 75% (1999-2003) compared to 1989-1993, exceeding 700,000 acres in 2004. This increase in production is not matched by an increase in market demand, resulting in depressed prices. One of the major objectives of research conducted at the University of Saskatchewan has been to find alternative uses for the crop. As a first step we bred out the potentially harmful trichomes (hairs) on the canaryseed hull. CDC Togo was the first glabrous canaryseed cultivar obtained from a planned cross. The first glabrous Canaryseed (Canario ^{TM}) cultivar, CDC Maria, is 10-15% lower yielding than pubescent-hull cultivars such as Keet and Elias (Hucl et al., 2001). We subsequently combined the glabrous trait with the yellow-seed trait. The intent of this proposal was, in part, to evaluate the agronomic performance of GY (glabrous-yellow) canaryseed lines. Yellow seeded, glabrous canaryseed cultivars will eventually be used in the food sector while brown seeded cultivars will be used in the traditional bird seed market. A second objective of this proposal was to evaluate the growth regulator ethrel as a potential gametocide as a crossing aid for canaryseed. The final objective was to identify molecular markers that might be useful in measuring hybridity when making crosses using either a gametocide or an approach-pollination protocol which results in both self-fertilized and cross-pollinated progeny.

Registration Testing:

The introduction of new Canaryseed cultivars is subject to CFIA regulations covering Cultivar Registration. Submissions are voted on by the Prairie Grain Development Committee-Special Crops Subcommittee. The Canaryseed Cooperative Test coordinated by AAFC was abolished in 1994. As a result data for cultivar registration testing was conducted on an ad-hoc basis post-1994. One source of data, the Saskatchewan Regional Variety Testing program run by the CDC and funded by the province of Saskatchewan was terminated in early 2003. Thus, data collection became even more of a challenge. As part of this project an annual Registration Test for Glabrous Canaryseed was developed and grown in 2006 and 2007. Protocols were established and subsequently approved by the PGDC.

A further objective of this project was to evaluate approximately 100 lines in 3-rep tests at three sites in 2005 and 2006 in order to feed lines into the Registration testing system. In addition

approximately 500 lines were to be evaluated in unreplicated yield trials at a single site in 2005 and 2006.

Gametocide-aided crossing of Canaryseed:

One of the basic requirements for conducting a mature breeding program is the ability to develop new populations for selection purposes. This requires the ability to cross-pollinate genotypes of a self-pollinating species such as *Phalaris canariensis*. Traditional crossing protocols used for cereals such as wheat, barley and oat do not work well for Canaryseed. Manual emasculation of the panicle results in very high rates of floret abortion. Our early attempts at manual emasculation and pollination were unsuccessful as were hot water treatments to destroy the pollen. Hot water treatments have been used successfully for a number of grass species. We resorted to using the approach method without emasculation and using morphological markers to identify hybrid plants. The success rate is typically around 1-2%. Subsequently we used a male gametocide utilized in hybrid wheat production. We were thus able to facilitate the development of Canaryseed populations for genetic studies (Matus-Cadiz et al., 2003). In the interim, production of the gametocide "Genesis" ceased with the termination of a number of hybrid wheat breeding efforts.

A growth regulator, "Ethrel", was shown to have male gametocide properties when applied to cereals. Ethrel has been tested as a male gametocide in barley, spring wheat, pearl millet, and Triticale. Ethrel was first used as a male gametocide in 1969 to increase the number of pistillate flowers in monoecious cucumbers (McMurray and Miller, 1969). Induction of floret sterility ranged from 54 to 99%. Percentage sterility is dependent on applying Ethrel at the correct growth stage and sufficient concentration (Hughes et al., 1974). Ethrel application is generally thought to be most effective if applied just before meiosis is initiated in the main tiller (Hughes et al., 1974). Recommended growth stages are generally pre-booting to early–booting (Zadoks growth stage [ZGS] 39 to 43). The effectiveness of Ethrel drops dramatically once meiosis is initiated or completed within tillers but higher levels of Ethrel have been shown to promote partial sterility within spikes (Hughes et al., 1974). Floret sterility of 80 to 99% has generally been achieved with Ethrel rates of 2000 to 3000 ppm. Usage of 2000 or 3000 ppm of Ethrel has been associated with (1) increased post-treatment tillering, (2) reduced plant height, (3) delayed pollination, and (4) poor spike emergence through the boot. Hughes et al (1976) suggested using 100 ppm of GA_3 to promote full emergence of male sterile spikes.

We initiated preliminary studies using ethrel on Canaryseed in 2003. Rates suggested for wheat were not appropriate for Canaryseed, resulting in excessive growth reduction and retardation. We subsequently fine-tuned the gametocide application protocol somewhat by testing a range of product concentrations in order to find a level resulting in partial male-sterility without apparent female sterility being induced in Canaryseed florets. We proposed to further develop the protocol to take into account crop staging at the time of ethrel application.

AFLPs and SSRs as molecular markers for hybridity confirmation:

The use of gametocides does not result in complete hybridity (ie self-pollinated seeds are set). Thus morphological or molecular markers are required to confirm whether seed from a cross is

in fact an F1 hybrid. We have been using hull pubescence and seed colour as morphological markers. Although those two markers have been useful in the initial breeding efforts, they have become a limiting step. We demonstrated that isozyme markers will differentiate canarygrass species but not individual accessions within a species (Matus and Hucl, 1999). Two small studies by Junk and Pozniak (unpublished) demonstrated that RAPD markers provide us with similar genetic resolution as isozyme markers. Thus, these two avenues are closed to us. For this project, we proposed to evaluate an array of AFLPs (Amplified Fragment Length Polymorphisms) and oat microsatellite (SSRs) primers on up to 10 canaryseed cultivars or accessions.
The AFLP technique produces highly complex DNA profiles by arbitrary amplification of restriction fragments ligated to double-stranded adaptors with hemi-specific primers harboring adaptor-complementary 5' termini (Vos et al., 1995). The technique has been widely used in the construction of genetic maps containing high densities of DNA marker loci. The AFLP protocol amplifies restriction fragments obtained by endonuclease digestion of target DNA using "universal" AFLP primers complementary to the restriction site and adapter sequence. However, not all restriction fragments are amplified because AFLP primers also contain selective nucleotides at the 3' termini that extend into the amplified restriction fragments. These arbitrary terminal sequences result in the amplification of only a small subset of possible restriction fragments. The number of amplified fragments (generally kept around 50-100) can therefore be "tailored" by extending the number of arbitrary nucleotides added to the primer termini. Alternatively, the use of endonuclease combinations that vary in their restriction frequency can also be used to tune the number of amplicons. Generally, the abundant restriction fragments produced from complex genomes require AFLP primers with longer selective regions. Conversely, analysis of small genomes require only few arbitrary nucleotides added at the primer 3' termini. The resulting AFLP fingerprints are usually a rich source of DNA polymorphisms that can be used in mapping and general fingerprinting endeavors.

A small set of existing oat SSRs were assessed for their transferability to canaryseed because canaryseed is taxonomically more closely related to oat (*Avena sativa*) than to wheat (*Triticim*) or barley (*Hordeum vulgare*).

METHODS AND RESULTS

METHODS:

Yield trials:

Field trials were conducted at the University of Saskatchewan Seed Farm, Kernen Crop Research Farm, IHARF, Viterra Watrous Research Farm and Swift Current Wheatland AgriArm (2005 and 2006) or AAFC SPARC (2007) typically using a 3 replication 6 x 6 Lattice design. The cultivars CDC Maria and CDC Togo along with experimental lines C99005 (yellow seeded glabrous prototype) and C99037 (= CDC Bastia) were included as controls. Standard small plot techniques were used with a seeding rate of 250 seeds/m2. Plot sizes varied across test institutions. Plots grown by the CDC program were 1.2 x 3.6 m in size and consisted of four rows spaced 0.3 m apart. Seed placed fertilizer (11-55-0) was applied at a rate of 50 kg/ha. Weed control was typically via the application of Buctril-M.

Test weights and kernel weights were measured on a cross-replicate composite. For each line grown in replicated trials a purification plot was grown at Saskatoon. Each purification plot was bordered with dwarf wheat to reduce panicle tangling and to provide a buffer between plots during the seeding process.

Gametocide experiment:

Ethrel was applied to CDC Togo plots at two growth stages (ZGS 32 or 41) and at three rates (900, 1200 and 1500 ppm). At heading 10 panicles per plot were harvested and stored in an alcohol-acetic acid fixative solution. Pollen from these 10 panicles was subsequently stained with KI to estimate pollen sterility (non-staining pollen grains). Ten panicles in each plot were covered with individual custom-made onion skin paper crossing bags to prevent cross-pollination. At maturity 10 bagged and 10 unbagged (open-pollinated) panicles per plot were analyzed for seed number and floret number. Days to heading, days to maturity and plant height were recorded for each plot. The plots were subsequently combine-harvested in order to determine grain yield. The experimental design was an RCBD with four replications. This experiment was grown at the University of Saskatchewan Seed Farm in both 2006 and 2007. Standard plot size and seeding rates were used. Ethrel was applied using a back-pack sprayer and hand-held spray boom.

AFLP and SSR molecular marker protocol development for canary seed hybridity determination:

The objective of this work was to identify AFLP (Tables 16 and 17) and oat microsatellite (Tables 18 and 19) primers that could be used to confirm a cross-pollination among any two of four canaryseed genotypes ('C04016', 'C03028', 'C03058', and 'C02074').

The four canaryseed genotypes included 'C04016', 'C03028', 'C03058', and 'C02074'. Pedigrees were as follows: C04016 = Cantate//CDC Maria/PI415822; C03028= C99005//Cantate*3/CDC Maria where C99005 is a glabrous yellow line with pedigree CDC Maria/CY184; C03058 (yellow seeded line) = CDC Maria/CY184//CY186 where CY lines were the original yellow pubescent mutants pulled out of the Keet bulk so C03058 is essentially a mutagenized version of 'Keet'; and C02074 (yellow seeded) = GY x Cantate/CDC Maria where GY stands for glabrous and yellow selection (i.e., CDC Maria x a CY line). The four canaryseed genotypes used in this study were used in the 2005 summer crossing block as follows: C03028 x C03058; C04016 x C02074; and C03028 x C02074 (all primer combos and gels were run with these comparisons in mind). All AFLP gels were scanned and archived as *.tif files and printed out. A closer look can be given to major and minor bands within the archived *.tif files using ALPHAEASE FC STAND ALONE (v 4.0). This program can also be used to generate dendrograms and a summary of band matching among genotypes. The band matching results can be inputted into NTSYS to generate a dendrogram over many primer sets. AFLP markers are dominant markers and thus a hybridization event (F1) will be identified on gels as a putative F1 by having the AFLP bands from parent 1 and parent 2 (ie AFLP bands in parent 1 + AFLP bands in parents 2 = AFLP genotype of F1 hybrid).

The AFLP protocol can be divided into the following steps: (1) DNA digestion with two different restriction enzymes (generally a rare and a frequent cutter), (2) ligation of double-stranded adapters to the ends of the restriction fragments, (3) optional DNA pre-amplification of ligated product directed by primers complementary to adapter and restriction site sequences, and (4) DNA amplification of subsets of restriction fragments using selective AFLP primers and labelling of amplified products. Amplification of very small "genomes" (plasmids, cosmids, BACs) requires primers with no selective nucleotides. AFLP fingerprinting of bacteria and fungi generally requires primers with 2 selective bases (eg., E-NN and M-NN). Complex genomes require the use of more than 2 selective bases in one or both primers. In the case of complex genomes it is recommended to carry the amplification in two consecutive steps (preamplification and selective amplification) to increase specificity and the amount of initial template. MseI/MseI, EcoR1/EcoR1, and EcoR1/MseI amplicons are all detected but the method favors the generation of primarily EcoR1/MseI amplicons. The generation of doublets resulting from the different mobility of complementary strands is expected. Finally, the reaction products are separated by electrophoresis using denaturing polyacrylamide gels and silver stained to visualize the AFLP fingerprints (Figure 1).

RESULTS

Registration Testing and selection of promising yellow seeded lines:

A summary for the 38 replicated trial yields conducted between 2005 and 2007 and their Coefficients of Variation (CV's) is presented in Table 1. Average site yields ranged from 365 to 2495 kg/ha with CV's ranging from a low of 4.3 to a high of 31.6%. Trials with CV's in excess of 15% were not included in the long-term database. On average, yields were highest in 2005 (1515 kg/ha) and dropped off by 20 and 25% in 2006 and 2007, respectively.

The results of the 2005 yield trials are reported in Tables 2 through 6. CDC Togo yielded 12% higher than CDC Maria in the 2005 Pre-Registration Test (Table 2) which is consistent with our long-term data. The brown-seeded line C00038 yielded 22% higher than CDC Maria in 2005. This line holds promise as a cultivar and we initiated breeder seed production in 2005. Of the 12 more promising lines in the 2005 Registration Test, eight were yellow-seeded. The lines C03040 and C03087 yielded slightly higher than CDC Togo but were later maturing by 2 to 3 days (Table 2).

In other replicated trials conducted in 2005 (Tables 3 to 6), an additional 37 promising yellow-seeded lines were identified.

The results of the 2006 yield trials are reported in Tables 7 through 11. The data from the 2006 Glabrous Canaryseed Registration Test is presented in Table 7. As was the case in 2005, glabrous yellow-seeded lines were competitive with the best brown-seeded lines. A significant number of promising lines were identified in the 2006 trials CANYT#2 and CANYT#3 but relatively few in CANYT#4 and 5. The latter two trials consisted mainly of lines from one cross (C00034/C02145) which produced later-maturing, tall and lower yielding progeny. The parent C02145 had performed very well under the 2002 mid-season drought pattern but poorly under terminal drought in 2003. Thus, it is not surprising that the progeny of this parent fared poorly in 2006.

In 2007, two replicated trials were grown. The first was the 2007 Glabrous Canaryseed Registration Test (Table 12). Of the five sites, three produced usable data. The GY lines C03087, C04035 and C05041 continued to perform well relative to the brown-seeded lines. The entries in the second trial (2007 CANYT#2) all yielded less than the check cultivars and were dropped from further testing. The data from that trial has not been included in this report.

Unreplicated yield testing of canaryseed breeding lines

Approximately 930, 250 and 1,500 glabrous lines were be evaluated in unreplicated yield trials at Kernen in 2005, 2006 and 2007, respectively. The retention rate ranged from 5 to 10% (Table 13).

Early generation breeding material

Early generation breeding activities for 2005 to 2007 are summarized in Table 14. The number of lines grown in hill plots in the F3 or F4 generations ranged from 4,400 to 9,600 during the course of this project. All this material had to be hand threshed and hand-planted in order to avoid mechanical seed mixing.

The 2005 F1 nursery was flooded twice and weed control was hampered. In excess of 46,000 seeds from 13 potential new crosses made in 2004 were hand space-planted. The maturity of the plants was delayed to the point that seed color could not be determined. These putative F2 populations were subsequently grown in bulk plots in 2006. Approximately 500 F2 panicles were harvested per plot and each panicle was checked for brown seed color and then bulked to produce an F3 bulk which was then planted in 2007.

Three new crosses were made in 2005 (Table 14). Ethrel was applied to the female parent at ZGS32. In excess of 1,000 plants were grown in the phytotron during the fall of 2005. The hybridity rate averaged 2.6% for the three crosses. The putative F2 populations were grown in the phytotron during the winter of 2005-2006 for advancement to F3 hills in 2006. The same gametocide protocol was used in 2006 with roughly the same hybridity level.

Breeder seed development of GY lines:

The development of breeder seed of the most promising food-grade (glabrous-yellow) canary seed experimental lines identified in 2003-2004 trials was initiated in 2005. The lines C00030 and C03058 were sown in 15 m long breeder strip plots using hand-picked seed from our 2004 purification plots. Individual panicles (n=250) were picked from the centre of each strip. We assessed the phenotype of each panicle then bulk-threshed the panicles to produce seed for an initial breeder plot in 2006. Neither of these lines was retained on the basis of our 2005 trials. In 2006, five GY lines were grown in 15 m purification strips: C03040, C03087, C05041, C05070 and C05091. In 2007 the line C03040 was dropped and breeder seed plots were sown for the

remaining four GY lines. The objective is to select the most promising two or three lines for further seed multiplication and to use them in studies towards new-uses for the crop.

Gametocide-aided crossing of Canaryseed:

Ethrel was applied to canary seed plots at ZGS 32 or 40 at either 900, 1200 or 1500 ppm (Table 8). Applying 1200 or 1500 ppm ethrel at ZGS32 resulted in 36-27% pollen sterility in 2005. This in turn reduced seed set with the 1200 ppm treatment while the 1500 ppm treatment did not reduce seed set. The partial sterility of panicles likely resulted in the fertile florets pollinating those that are sterile; hence the lack of reduction in seed numbers per panicle. Ethrel delayed heading by up to 5 days. This delay carried through to maturity. Plant height was reduced by up to 17 cm. Grain yields were reduced, but the reductions were not statistically significant.

In 2006, ethrel application resulted in pollen sterility levels ranging from 45 to 74% (ns) compared to an average of 10% in 2005. The 2006 control plots experienced sterility levels averaging 43%. Thus the environmental conditions encountered in 2006 resulted in high pollen sterility levels with and without ethrel application. The 2006 control plot yields, seed and floret numbers per panicle were nearly half of those observed in 2005 (Table 8). Grain yield of ethrel-treated plots decreased by up to 90% relative to the control (P=0.05). The yield reduction was twice as large for plots treated at the later plant stage (ZGS 40). As was the case in 2005, ethrel delayed heading, flowering and maturity while reducing plant height. The % seed set for bagged panicles was reduced by nearly half with the ZGS40 ethrel treatments in 2006. In 2005 no reduction was observed at either the ZGS32 or ZGS40 application stages. Similarly, the non-bagged (OP= Open Pollinated) panicles showed no reduction in % seed set with ethrel treatment in 2005 while in 2006 the ZGS40 applications resulted in a 20% unit drop in seed set. In comparing the bagged versus OP panicles for the 2005 experiment, the OP panicles had a 16% higher seed set while in 2006 they had a 20% higher seed set. This suggests that cross-pollination occurred in the OP panicles or that the bagging of panicles resulted in heat stress that caused seed abortion. However, the control treatment panicles did not show as pronounced a difference in % seed set between the bagged and OP panicles in 2006 as did the ZGS40 treatments, suggesting that the ethrel treatment did have an effect on self-pollination.

In conclusion, ethrel does not appear to be an effective gametocide in canaryseed as we still obtained up to 31% seed set with the later application of the compound and no significant difference from the control for the ZGS32 application in 2006. In 2005, the ethrel-treated plots did not differ from the control in seed set for bagged and OP panicles.

AFLP and SSR molecular marker protocol development for canary seed hybridity determination:

Out of 16 EcoRI x 16 MseI AFLP selective primer combinations = 256 possible combinations approximately 255 possible primer combinations were screened (99.6 %) during the first six months of this project (Tables 16 and 17). One AFLP primer combo E5-M7 (E5= GACTGCGTACCAATTC**ACG** and M7= GATGAGTCCTGAGTAA**CTG**) appeared to clearly differentiate among all four parental genotypes (Figure 1A) and thus might be used to detect putative F1 embyros derived using the contact pollination method. If no PCR products were

visualized from the sel-amps on agarose gels then it was expected that no bands would be evident on stained AFLP gels. Approximately 62 primer combos out of the 255 screened were identified from archived gels using ALPHAEASE FC STAND ALONE to possess sufficient polymorphism to merit a second screening.

A small set of existing oat SSRs were assessed for their transferability to canaryseed because RAPD research (Junk and Pozniak, unpublished) indicated that the canaryseed genome was more closely related to oats (*Avena sativa*) than to wheat (*Triticim*) or barley (*Hordeum vulgare*). Of 109 oat SSR primers (Table 18) tested on CDC Maria about 21 primers did not amplify a band of interest (equal to or <300 base pairs). Of the remaining primers, 72 primers required PCR conditions with a touchdown annealing temperature range of 46 to 40 C, seven primers required 53 to 40C while nine primers required 62 to 40C (Table 18). These results indicated that primer specificity was generally poor and thus the transferability of oat SSRs to canaryseed was poor.

The PCR products from a subset of primers were tested on 2.5% agarose gels and then 3% metaphor gels using 10 canaryseed parents. Primers AM106, AM109, AM15 (Table 18) showed promise and thus a subset of F2s and selfed plants were screened with their respective parents. The polymorphisms did not segregate as expected. AM109 did show some promise with a faint band <100 bp but canaryseed specific primers would likely have to be generated in order to allow for a definite conclusion. A re-evaulation of these three primer set in canaryseed is recommened using an automated DNA genetic analyzer.

Although canaryseed DNA extraction and processing was not problematic, the results were not reproducible and band presence or absence was very sensitive to PCR conditions. Based on the literature the next avenue would be to develop canaryseed specific microsatellite markers. This task was, however, beyond the scope of this project.

Conclusions and Recommendations

After three years of field evaluation using a series of 38 trials one can conclude that it is possible to develop glabrous-yellow (GY) seeded lines that are equal in performance to glabrous brown seeded cultivars like CDC Togo and CDC Bastia. The four most promising GY lines (C03087, C05041, C05070 and C05091) yielded (averaged over the 3 years or 9 to 15 station-years) 11 to 19% higher than CDC Maria or 3 to 10% higher than CDC Togo.

The next step will be to multiply seed of the most promising GY canaryseed lines for Novel Food evaluations and future release as cultivars.

In conclusion, the growth regulator ethrel does not appear to be an effective gametocide in canaryseed as we obtained incomplete male sterility and up to 31% seed set with the most effective concentration- plant stage combination in one of the two years. Thus, alternative approaches to creating male sterility in canaryseed will have to be explored in future research.

Canaryseed specific molecular markers which enable high-through put screening are currently lacking. Of the 255 AFLP combinations, 62 primer combinations showed sufficient polymorphism to merit further analysis. However, the level of variability between and/or among

parental lines of interest would need to be sufficiently high to merit the labor intensive and time consuming nature of conducting AFLP analyses. Furthermore, variable AFLP fragments from marker combinations (e.g., E-ACG/M-CTG) can be cloned, sequenced, and converted into sequence characterized amplified region (SCAR) markers (Orr and Molnar, 2007). These can be developed and subsequently used within the breeding program to confirm F1 hybridity in canaryseed.

In the long term, the development of canaryseed specific SSR markers is an important objective for this breeding program. Identifying SSRs with good polymorphic information content (PIC) will offer the program a rapid and high-through put molecular marker method, unlike AFLP markers, to confirm F1 hybridity. Of the 109 oat SSR markers assessed only three SSRs (3%) appeared to detect polymorphisms among the canaryseed lines tested. Unfortunately, this calls into question the transferability of oat SSRs to canaryseed. Generally, transferability of SSRs across genomes was expected to be at best 10 to 20%. However, current literature is suggesting that transferability may be higher than once expected (Zhang et al., 2005). In addition, the limited number of oat SSRs (n=109) that were available for study in 2005 generally had low PICs (grand averages = 0.51 to 0.57, Li et al., 2000) indicating that many of the SSRs were monomorphic (57% =19 polymorphic SSRs/44 total SSRs * 100, Li et al 2000) and, thereby, of little informative value within oats. Thus, at this point, it is likely that low PIC values for the oat SSRs tested, instead of low transferability, likely contributed the most to our low success rate with oat SSRs in canaryseed. Numerous groups still continue to identify new oat SSRs for breeding and mapping efforts (Brautigam et al., 2005, Hu et al., 2007). A large number of oat ESTs have been identified in recent years and thus as useful oat SSRs become available it is recommended that oat SSRs with high PIC values (no. of alleles ≤ 8) be screened for transferability in canaryseed. In the long term, canaryseed specific SSR markers need to be identified and amassed similar to oat SSRs development over the past ten years (Li et al., 2000; Pal et al., 2002; Becher, 2007).

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Acknowledgements

I would like to thank the cooperators who conducted the Glabrous Canaryseed Registration Tests: W. May (IHARF), K. Hanson (Viterra Watrous), J. Payne/R. DePauw (AAFC SPARC) and B. Nybo (Wheatland Conservation Area Inc.)

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Equipment: None purchased for this project.
Project Developed Materials: Nil.
Expense statement: under separate cover from University of Saskatchewan Financial Services.

Table 1. Canaryseed yield trial summaries 2005-2007

Yield Trial and site	Yield trial average yield kg/ha	CV %	REPS #	entries #
05CANYT1-Seed Farm D1	2495	4.3	3	36
05CANYT1-Seed Farm D2	1941	8.2	3	36
05CANYT1-Kernen	1249	8.4	3	36
05CANYT1-Watrous	1581	9.2	3	36
05CANYT1-INDHD	2379	6.1	3	36
05CANYT1-SWCU	585	11.3	3	36
05CANYT2-Seed Farm	1966	6.6	3	36
05CANYT2-Kernen	1168	13.8	3	36
05CANYT2-SWCU	540	10.6	3	36
05CANYT3-Seed Farm	2086	10.6	3	36
05CANYT3-Kernen	1102	12.5	3	36
05CANYT3-SWCU	458	16.7	3	36
05CANYT4-Seed Farm	2409	6.2	3	36
05CANYT4-Kernen	1271	9.8	3	36
05CANYT5-Seed Farm	2117	6.9	3	36
05CANYT5-Kernen	892	13.1	3	36
06CANYT1-Seed Farm D1	1060	10.2	3	36
06CANYT1-Seed Farm D2	1059	12.1	3	36
06CANYT1-Kernen	1149	8.1	3	36
06CANYT1-Watrous	1037	11.9	3	36
06CANYT1-INDHD	1746	5.7	3	36
06CANYT1-SWCU	365	30.9	3	36
06CANYT2-Seed Farm	1311	10.5	3	36
06CANYT2-Kernen	1269	6.4	3	36
06CANYT2-Watrous	1076	10.1	3	36
06CANYT3-Seed Farm	1435	8.7	3	36
06CANYT3-Kernen	1189	8.8	3	36
06CANYT4-Seed Farm	1596	5.2	3	36
06CANYT4-Kernen	1114	7.8	3	36
06CANYT5-Seed Farm	1653	5.4	3	36
06CANYT5-Kernen	1072	9.5	3	36
07CANYT1-Seed Farm D1	1260	15.0	3	20
07CANYT1-Seed Farm D2	451	31.6	3	20
07CANYT1-Kernen	1319	7.1	3	20
07CANYT1-Watrous	1457	9.4	3	20
07CANYT1-SWCU	857	16.1	3	20
07CANYT2-Seed Farm	1394	12.1	2	17
07CANYT2-Kernen	1377	8.8	3	17
Average yield 38 SY	**1329**			

Table 2. Agronomic performance of selected lines evaluated in trial 2005 CANYT#1

ENTRY	NAME		Yield	DSE	DPM	ht	twt	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.0	0.00	GB
2	C99005	Maria x CY184	108.1	1.4	2.3	1.7	0.2	0.29	GY
3	C99037	Maria x CY184	105.4	1.1	2.4	0.0	1.1	0.33	GB
4	CDC Togo	Cantate x Maria	112.4	1.1	3.0	-0.3	-0.4	1.05	GB
6	C00038	Maria x 46	121.7	1.1	2.0	-3.5	-1.1	0.19	GB
14	C03040	C99005//Cant*3/Maria	114.4	2.7	5.1	1.8	0.7	0.81	GY
19	C03087	Cantate*2/Maria//CY186	116.0	4.8	5.8	-2.6	0.5	1.04	GY
22	C04016	Cantate/Maria x 50	120.7	3.9	4.8	4.2	0.8	-0.24	GB
23	C04020	Cantate*3/Maria	118.3	2.0	4.8	-0.8	-0.8	0.88	GB
25	C04025	C99005//Cantate*3/Maria	119.0	2.9	5.1	-3.7	0.6	0.82	GB
28	C04035	Maria/CY184//CY186	121.1	3.0	4.8	6.4	-0.3	0.47	GY
29	C04037	C99005//Cantate*3/Maria	115.5	1.3	3.3	1.4	-0.3	0.67	GY
30	C04040	Maria/CY184//CY186	115.8	5.4	5.1	0.3	-0.6	0.23	GY
31	C04044	Maria/CY184//CY186	115.2	2.4	3.8	4.3	0.3	0.43	GY
33	C04055	Maria/CY184//CY186	114.7	4.6	4.4	4.0	0.1	0.27	GY
34	C04057	C99005/C99025	114.3	3.9	4.7	1.8	-0.7	0.71	GY
		# of sites	6	5	4	5	4	4	

GB = glabrous brown, GY = glabrous yellow. Yield is expressed as a % of CDC Maria other traits are expressed as a deviation from CDC Maria. DPE = days to 50% panicle emergence, DTM = days to maturity, twt = test weight (kg/hL), kwt = kernel weight (mg)

Table 3. Agronomic performance of selected lines evaluated in trial 2005 CANYT#2

ENTRY	NAME		Yield	DSE	DPM	ht	twt	kwt	seed
1	CDC Maria		**100.0**	0.0	0.0	0.0	0.0	0.0	GB
2	C99005	Maria x CY184	**116.5**	1.4	0.6	-0.6	0.6	0.1	GY
3	C99037	Maria x CY184	**115.5**	1.0	0.1	1.2	0.6	0.0	GB
4	CDC Togo	Cantate x Maria	**119.8**	1.6	1.2	-1.0	0.5	0.8	GB
5	C04062	C99005/C99025	**121.7**	2.3	2.2	2.9	0.1	0.4	GY
13	C05002	Cantate*5/Maria	**123.4**	2.6	3.3	-6.8	-1.0	1.2	GB
14	C05003	Cantate*5/Maria	**135.9**	2.1	1.0	-5.7	-0.6	0.9	GB
15	C05004	Cantate*5/Maria	**137.8**	-0.8	0.9	-7.2	-1.2	0.2	GB
16	C05005	Cantate*5/Maria	**123.7**	2.9	3.2	-5.1	0.7	1.0	GB
19	C05008	Cantate*5/Maria	**121.6**	2.4	1.6	-3.0	-0.1	1.0	GB
23	C05012	Cantate*5/Maria	**121.8**	3.0	2.5	-4.2	-0.4	1.1	GB
24	C05013	Cantate*5/Maria	**122.2**	3.0	2.2	-6.3	0.1	1.1	GB
26	C05015	Cantate*5/Maria	**122.1**	2.0	1.6	-1.6	0.7	0.7	GB
32	C05021	Cantate*4/Maria//368984	**131.9**	1.8	1.8	-1.7	0.2	0.4	GB
33	C05022	Cantate*4/Maria//368984	**126.9**	1.7	1.8	-2.4	0.1	0.7	GB
35	C05024	C99005//Cantate*4/Maria	**123.5**	1.9	2.4	-4.2	0.5	0.7	GY
36	C05025	C99005//Cantate*4/Maria	**125.9**	2.0	1.9	0.4	1.0	0.6	GY
		# of sites	3	2	2	2	2	2	

Table 4. Agronomic performance of selected lines evaluated in trial 2005 CANYT#3

ENTRY	NAME		Yield	DSE	DPM	ht	twt	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.0	0.0	GB
2	C99005	Maria x CY184	105.4	1.5	1.4	-1.2	-0.1	0.0	GY
3	C99037	Maria x CY184	100.9	1.4	0.4	1.5	0.9	0.0	GB
4	CDC Togo	Cantate x Maria	110.4	1.8	0.2	-0.6	-0.2	0.5	GB
6	C05027	C99005//Cnt*4/Mr	109.6	1.7	1.6	-6.0	0.5	0.2	GY
7	C05028	C99005//Cnt*4/Mr	110.3	2.8	3.5	-5.1	0.1	0.6	GY
10	C05031	C99005//Cnt*4/Mr	108.3	1.8	2.1	-5.7	0.2	0.6	GY
16	C05037	C99005//Cnt*4/Mr	116.7	3.0	1.3	-3.8	0.7	0.2	GY
17	C05038	C99005//Cnt*4/Mr	118.4	2.1	1.7	0.1	1.1	0.6	GY
20	C05041	C99005//Cnt*4/Mr	122.1	1.4	1.6	-2.8	1.2	0.0	GY
22	C05043	C99005//Cnt*4/Mr	117.6	1.7	0.9	-7.2	-0.4	-0.1	GY
24	C05045	C99005//Cnt*4/Mr	112.5	1.6	1.8	-3.2	1.0	0.4	GY
25	C05046	C99005//Cnt*4/Mr	112.2	2.0	2.6	-2.4	1.1	0.3	GY
32	C05053	C99005//Cnt*4/Mr	112.8	1.4	1.8	-3.3	0.2	-0.1	GY
35	C05056	C99005//Cnt*4/Mr	113.9	1.3	1.3	-0.6	0.0	0.0	GY
36	C05057	C99005//Cnt*4/Mr	118.1	2.1	1.3	1.1	0.5	0.2	GY
		# of sites	2	2	2	2	2	2	

Table 5. Agronomic performance of selected lines evaluated in trial 2005 CANYT#4

ENTRY	NAME		Yield	DSE	DPM	ht	twt	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.0	0.0	GB
2	C99005	Maria x CY184	109.0	1.4	-0.3	0.2	0.8	0.2	GY
3	C99037	Maria x CY184	116.2	1.5	0.7	2.8	0.9	0.2	GB
4	CDC Togo	Cantate x Maria	123.3	1.3	0.1	-1.2	0.4	0.9	GB
8	C05061	C99005//Cnt*4/Mr	125.7	1.6	1.7	1.2	1.1	0.8	GY
10	C05063	C99005//Cnt*4/Mr	122.6	1.7	1.4	1.8	1.2	0.9	GY
11	C05064	C99005//Cnt*4/Mr	125.7	2.2	0.9	-2.7	0.6	0.5	GY
12	C05065	C99005//Cnt*4/Mr	125.4	2.3	1.2	0.6	1.8	1.0	GY
13	C05066	C99005//Cnt*4/Mr	126.5	2.0	1.5	-1.2	1.3	0.7	GY
17	C05070	C99005//Cnt*4/Mr	123.5	1.9	1.0	-4.1	0.1	0.5	GY
24	C05077	C99005//Cnt*4/Mr	134.5	2.6	1.6	-3.5	1.5	1.0	GY
25	C05078	C99005//Cnt*4/Mr	130.7	2.4	1.0	1.8	1.2	1.0	GY
26	C05079	C99005//Cnt*4/Mr	123.6	1.8	1.9	-4.9	1.3	0.8	GY
27	C05080	C99005//Cnt*4/Mr	128.6	2.5	1.5	-0.7	1.5	1.1	GY
28	C05081	C99005//Cnt*4/Mr	124.1	1.9	1.4	-0.8	0.7	0.8	GY
29	C05082	C99005//Cnt*4/Mr	132.6	2.7	3.1	-2.3	0.5	1.2	GY
30	C05083	C99005//Cnt*4/Mr	127.2	2.5	1.3	1.5	1.6	0.8	GY
31	C05084	C99005//Cnt*4/Mr	123.4	4.0	3.5	-4.1	1.2	0.8	GY
34	C05087	C99005//Cnt*4/Mr	124.5	1.7	1.4	-2.0	0.1	0.7	GY
36	C05089	C99005//Cnt*4/Mr	124.6	2.4	1.8	-3.6	2.1	1.1	GY
		# of sites	2	2	2	2	2	2	

Table 6. Agronomic performance of selected lines evaluated in trial 2005 CANYT#5

ENTRY	NAME		Yield	DSE	DPM	ht	twt	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.0	0.00	GB
2	C99005	Maria x CY184	117.1	2.2	0.7	2.7	0.8	0.12	GY
3	C99037	Maria x CY184	118.0	1.7	1.9	3.4	1.0	0.18	GB
4	CDC Togo	Cantate x Maria	116.1	2.4	0.7	-0.9	-0.2	0.76	GB
5	C05090	C99005//Cnt*4/Mr	123.7	2.6	2.4	0.3	0.8	0.70	GY
6	C05091	C99005//Cnt*4/Mr	142.9	3.2	2.7	1.7	1.2	0.72	GY
9	C05094	C99005/C99025	125.7	3.1	1.5	2.2	0.6	0.44	GY
14	C05099	C99005/C99025	123.8	3.2	1.8	4.2	0.2	0.68	GY
16	C05101	C99005/C99025	127.2	3.0	1.6	3.5	-0.3	0.58	GY
18	C05103	C99005/C99025	128.3	3.4	2.9	7.2	0.8	0.92	GY
19	C05104	C99005/C99025	125.4	3.1	1.3	2.9	0.7	0.36	GY
20	C05105	C99005/C99025	121.9	3.3	2.8	2.5	0.4	0.86	GY
21	C05106	C99005/C99025	125.1	2.8	2.1	2.1	0.9	0.56	GY
22	C05107	C99005/C99025	128.7	2.7	1.6	5.0	1.5	0.54	GY
24	C05109	C99005/C99025	127.2	3.4	2.5	1.8	0.7	0.58	GY
28	C05113	C99005/C99025	127.3	3.1	1.6	4.0	0.8	0.64	GY
32	C05117	C99005/C99025	123.4	3.4	2.0	3.7	0.4	1.12	GY
33	C05118	Cantate*4/Maria	128.1	3.1	3.2	-5.4	-0.5	1.08	GB
34	C05119	Cantate*4/Maria	122.8	3.2	2.8	0.0	-0.8	1.46	GB
36	C05121	Cantate*4/Maria	124.5	3.4	3.1	-1.6	1.0	0.82	GB
		# of sites	2	2	2	2	2	2	

Table 7. 2006 Glabrous canaryseed Registration Test - Summary of selected lines

ENTRY	NAME	Pedigree	Yield kg/ha	Heading days	Maturity days	Height cm	Lodging 1 to 9	Test wt. kg/hL	Seed wt. mg
1	CDC Maria		1239	54.0	87.2	97.9	3.7	71.6	7.52
2	C99005	Maria x CY184	1347	51.9	85.5	95.4	2.0	71.2	7.72
3	C99037	Maria x CY184	1332	53.9	87.0	100.2	3.3	71.5	7.65
4	CDC Togo	Cantate x Maria	1269	53.3	87.6	92.5	2.7	70.4	8.25
5	C00038	Maria x 46	1348	54.0	86.4	93.5	3.0	69.8	7.59
7	C03087	Cantate*2/Maria//CY186	1308	53.8	89.1	96.6	2.3	70.5	8.13
9	C04035	Maria/CY184//CY186	1376	55.0	87.8	103.7	3.0	70.6	8.06
14	C05003	Cantate*5/Maria	1269	51.4	87.4	88.5	1.3	70.2	8.17
15	C05004	Cantate*5/Maria	1418	50.3	85.0	92.5	1.3	69.9	7.53
21	C05021	Cantate*4/Maria//368984	1217	50.9	87.2	91.4	1.7	70.4	7.94
22	C05022	Cantate*4/Maria//368984	1249	50.5	86.8	89.4	1.3	70.2	8.22
26	C05028	C99005//Cantate*4/Maria	1339	51.1	89.7	91.4	2.3	70.5	8.32
30	C05041	C99005//Cantate*4/Maria	1306	53.4	87.2	88.1	1.3	71.5	8.00
33	C05046	C99005//Cantate*4/Maria	1308	50.7	87.9	91.2	1.0	71.4	8.35
36	C05057	C99005//Cantate*4/Maria	1263	53.5	86.7	95.8	1.7	70.7	7.80
		#sites	5	4	5	5	1	5	5

Table 8. Agronomic performance of selected lines evaluated in trial 2006 CANYT#2

ENTRY	NAME		Yield	DSE	DPM	ht	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.00	GB
2	C99005	Maria x CY184	104.5	-0.3	0.3	1.5	0.12	GY
3	C99037	Maria x CY184	103.4	-0.1	1.3	4.5	0.29	GB
4	CDC Togo	Cantate x Maria	96.7	-0.5	1.4	-0.8	0.67	GB
5	C05061	C99005//Cantate*4/Maria	104.0	-2.2	1.5	-0.4	0.67	GY
8	C05065	C99005//Cantate*4/Maria	112.7	-2.1	1.7	2.2	0.61	GY
10	C05070	C99005//Cantate*4/Maria	105.5	0.0	1.4	-1.0	0.17	GY
16	C05082	C99005//Cantate*4/Maria	112.5	-2.1	2.9	-4.1	0.71	GY
20	C05089	C99005//Cantate*4/Maria	113.7	-1.9	2.4	-3.2	0.6	GY
21	C05090	C99005//Cantate*4/Maria	115.4	-2.5	1.4	-1.6	0.5	GY
22	C05091	C99005//Cantate*4/Maria	112.2	-1.9	1.6	-2.1	0.69	GY
34	C05118	Cantate*4/Maria	98.1	-1.9	2.2	-8.3	1.23	GB
35	C05119	Cantate*4/Maria	104.1	-1.7	2.1	-1.9	1.07	GB
		# sites	3	3	3	3	3	

Table 9. Agronomic performance of selected lines evaluated in trial 2006 CANYT#3

ENTRY	NAME		Yield	DSE	DPM	ht	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.00	GB
2	C99005	Maria x CY184	103.7	-0.8	1.3	-0.1	0.32	GY
3	C99037	Maria x CY184	110.0	-0.5	0.6	4.6	0.41	GB
4	CDC Togo	Cantate x Maria	102.6	-1.4	0.2	-1.7	0.69	GB
5	C06001	Cantate*4/Maria//368984	111.8	-4.6	-1.2	-2.3	0.72	GB
6	C06002	Cantate*4/Maria//368984	110.4	-4.3	0.1	-3.4	0.52	GB
7	C06003	C99005//Cantate*4/Maria	114.9	-0.8	0.6	-5.7	0.36	GY
10	C06006	C00034/C02145	106.6	-0.1	2.3	1.3	0.15	GY
12	C06008	C00034/C02145	115.0	-1.3	0.2	4.4	-0.15	GY
13	C06009	C00034/C02145	111.6	-1.0	-0.1	5.4	-0.06	GY
16	C06012	C00034/C02145	112.7	-0.6	0.1	3.1	-0.09	GY
20	C06016	C00034/C02145	118.7	-0.5	2.0	5.0	0.30	GY
32	C06028	C00034/C02145	110.2	-0.8	0.7	2.6	0.10	GB
		# of sites	2	2	2	2	2	

Table 10. Agronomic performance of selected lines evaluated in trial 2006 CANYT#4

ENTRY	NAME		Yield	DSE	DPM	ht	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.00	GB
2	C99005	Maria x CY184	117.2	-2.4	-1.8	-1.4	0.00	GY
3	C99037	Maria x CY184	106.1	-0.2	1.4	3.3	-0.12	GB
4	CDC Togo	Cantate x Maria	102.6	-0.8	-0.6	-0.9	0.59	GB
14	C06042	C00034/C02145	114.7	-1.0	-1.0	2.7	-0.10	GY
31	C06059	C00034/C02145	112.6	-2.0	-1.1	2.5	0.09	GY
		# of sites	2	2	2	2	2	

Table 11. Agronomic performance of selected lines evaluated in trial 2006 CANYT#5

ENTRY	NAME		Yield	DSE	DPM	ht	kwt	seed
1	CDC Maria		100.0	0.0	0.0	0.0	0.00	GB
2	C99005	Maria x CY184	98.6	-2.5	-1.0	-3.5	0.34	GY
3	C99037	Maria x CY184	95.9	-0.1	0.2	1.2	0.15	GB
4	CDC Togo	Cantate x Maria	100.8	-0.7	1.2	-2.4	0.63	GB
17	C06077	C00034/C02145	105.0	-0.4	0.9	2.3	0.18	GY
		# of sites	2	2	2	2	2	

Table 12. 2007 Glabrous canaryseed Registration Test - Summary

ENTRY	NAME	Yield kg/ha	% Maria	Heading days	Maturity days	Height cm	Test wt. kg/hL	Seed wt. mg	seed
1	CDC Maria	1252	**100.0**	55.3	86.2	93.7	69.4	7.7	GB
2	C99005	1264	**101.0**	57.0	87.0	93.9	69.1	8.0	GY
3	CDC Bastia	1310	**104.6**	55.1	86.9	95.6	69.8	7.7	GB
4	CDC Togo	1421	**113.5**	55.6	87.2	94.8	68.1	8.5	GB
5	C00038	1346	**107.5**	56.7	86.6	88.0	68.0	7.8	GB
6	C03087	1385	**110.6**	58.9	88.4	97.6	68.8	8.5	GY
7	C04035	1424	**113.7**	57.6	87.1	101.3	69.0	8.1	GY
8	C05004	1343	**107.2**	54.6	86.7	92.3	67.8	7.6	GB
9	C05028	1462	**116.8**	56.7	89.6	93.2	69.3	8.6	GY
10	C05041	1496	**119.5**	57.4	87.4	88.3	70.0	8.0	GY
11	C05046	1326	**105.9**	55.2	87.7	90.3	69.9	8.2	GY
12	C05065	1279	**102.2**	55.1	87.4	95.5	*	*	GY
13	C05070	1400	**111.8**	56.7	87.3	91.1	69.2	7.9	GY
14	C05082	1376	**109.9**	56.2	88.1	93.9	69.1	8.5	GY
15	C05089	1156	**92.3**	56.9	87.9	89.3	*	*	GY
16	C05090	1429	**114.1**	56.1	87.7	95.1	70.0	8.3	GY
17	C05091	1433	**114.4**	56.1	87.4	93.6	70.2	8.2	GY
18	C05118	1153	**92.1**	56.3	88.6	87.9	*	*	GB
19	C06003	1432	**114.3**	57.2	87.4	91.4	69.3	8.0	GY
20	C06059	1221	**97.5**	56.2	86.3	97.6	*	*	GY
	# Sites	3		3	3	3	3	3	

Table 13. Inventory of lines undergoing initial, unreplicated testing (2005-2007)

2007 Lines planted no.	2007 Lines retained no.	2007 retained %	2006 Lines planted no.	2006 Lines retained no.	2006 retained %	2005 Lines planted no.	2005 Lines retained no.	2005 retained %
1581	129	8.2	248	13	5.2	930	96	10.3

Table 14 . Summary of early generation material 2005-2007

	2005	2005 no. populations	2006	2006 no. populations	2007	2007 no. populations
	no.		no.		no.	
Hills	4400	24	6631	28	9588	13
Bulks	0	0	143	14	79	12
New crosses		3		6		0

2005 hybridity results

Female			Male		# hybrid plants	Total plants	% hybridity
C02074	GY	X	C03028	GB	10	346	2.89
C02074	GY	X	C04016	GB	8	347	2.31
C03058	GY	X	C03028	GB	10	372	2.69
				Total	**28**	**1065**	**2.63**

Table 15. Effect of ethrel concentration and time of application on canaryseedseed production in each of two years at Saskatoon

2005

TRT		Yield kg/ha	Days to head	5% anthesis	95% anthesis	Days to maturity	Height cm	Pollen sterility %	bagged panicles no. seeds	bagged panicles no. florets	bagged panicles % seed set	OP panicles no. seeds	OP panicles no. florets	OP panicles % seed set
1	CONTROL 0	2060	60.8	62.0	65.5	102.5	107.8	0.1	69	111	62	88	114	77.1
2	ZGS32 900	1895	62.5	63.8	67.8	104.8	100.8	1.8	62	107	582	79	110	72.4
3	ZGS32 1200	1880	63.5	65.0	68.8	105.8	95.5	25.7	53	108	49	85	114	74.5
4	ZGS32 1500	1654	63.5	65.5	69.3	106.3	94.3	27.2	67	106	62	77	109	70.7
5	ZGS40 900	1635	64.5	66.8	70.3	105.5	94.3	0.3	55	107	51	79	115	69.2
6	ZGS40 1200	1919	64.8	68.8	72.5	106.3	90.5	11.3	64	102	62	75	127	74.5
7	ZGS40 1500	1673	65.0	68.8	72.3	106.5	93.0	4.2	63	116	54	85	125	68.3
	Average	1817	63.5	65.8	69.5	105.4	96.6	10.1	62	108	56.8	81	116	72.4
		ns	**	**	**	**	**	**	ns	ns	ns	**	ns	ns
	LSD		0.9	0.9	1.2	1.1	4.5	15.1				6		

2006

TRT		Yield kg/ha	Days to head	5% anthesis	95% anthesis	Days to maturity	Height cm	Pollen sterility %	bagged panicles no. seeds	bagged panicles no. florets	bagged panicles % seed set	OP panicles no. seeds	OP panicles no. florets	OP panicles % seed set
1	CONTROL 0	1114	52.0	55.0	58.0	85.5	92.3	43.2	32	64	50	57	80	70.5
2	ZGS32 900	725	55.0	57.0	60.3	88.5	65.8	65.6	41	71	58	57	76	74.6
3	ZGS32 1200	489	54.8	58.3	62.0	89.3	64.0	59.4	35	73	47	52	74	69.1
4	ZGS32 1500	579	55.5	57.0	60.3	89.3	63.0	45.3	37	66	56	51	74	68.7
5	ZGS40 900	293	57.0	60.0	64.5	92.3	60.0	63.6	19	58	31	36	62	58.1
6	ZGS40 1200	181	57.8	61.3	66.0	92.5	57.3	74.4	18	63	28	29	54	52.6
7	ZGS40 1500	131	59.8	62.3	66.5	92.5	56.3	52.9	14	54	27	23	54	42.9
	Average	502	56.0	58.7	62.5	90.0	65.5	57.7	28	64	42	43	68	62.3
		**	**	**	**	**	**	ns	**	ns	**	**	**	**
	LSD	218	1.8	1.2	1.7	1.4	5.1		15		18	14	14	8.3

Table 16. Code for 16 E-ANN and 16 M-CNN primers used for selective amplifications, for EcoR1+1A and MseI-+1C primers used for pre-amplifications, and adapter sequences which correspond to gDNA digested with EcoR1 and MseI restriction enzymes.

Universal code	Primer name	Sequence 5'-->3'
E1 or E-AAC	AFLPEcoRI-1	GACTGCGTACCAATTC**AAC**
E2 or E-AAG	AFLPEcoRI-2	GACTGCGTACCAATTC**AAG**
E3 or E-ACA	AFLPEcoRI-3	GACTGCGTACCAATTC**ACA**
E4 or E-ACC	AFLPEcoRI-4	GACTGCGTACCAATTC**ACC**
E5 or E-ACG	AFLPEcoRI-5	GACTGCGTACCAATTC**ACG**
E6 or E-ACT	AFLPEcoRI-6	GACTGCGTACCAATTC**ACT**
E7 or E-AGC	AFLPEcoRI-7	GACTGCGTACCAATTC**AGC**
E8 or E-AGG	AFLPEcoRI-8	GACTGCGTACCAATTC**AGG**
E9 or E-AAA	AFLPEcoRI-9	GACTGCGTACCAATTC**AAA**
E10 or E-AGA	AFLPEcoRI-10	GACTGCGTACCAATTC**AGA**
E11 or E-AAT	AFLPEcoRI-11	GACTGCGTACCAATTC**AAT**
E12 or E-AGT	AFLPEcoRI-12	GACTGCGTACCAATTC**AGT**
E13 or E-ATA	AFLPEcoRI-13	GACTGCGTACCAATTC**ATA**
E14 or E-ATC	AFLPEcoRI-14	GACTGCGTACCAATTC**ATC**
E15 or E-ATG	AFLPEcoRI-15	GACTGCGTACCAATTC**ATG**
E16 or E-ATT	AFLPEcoRI-16	GACTGCGTACCAATTC**ATT**
M1 or M-CAA	AFLPMseI-1	GATGAGTCCTGAGTAA**CAA**
M2 or M-CAC	AFLPMseI-2	GATGAGTCCTGAGTAA**CAC**
M3 or M-CAG	AFLPMseI-3	GATGAGTCCTGAGTAA**CAG**
M4 or M-CAT	AFLPMseI-4	GATGAGTCCTGAGTAA**CAT**
M5 or M-CTA	AFLPMseI-5	GATGAGTCCTGAGTAA**CTA**
M6 or M-CTC	AFLPMseI-6	GATGAGTCCTGAGTAA**CTC**
M7 or M-CTG	AFLPMseI-7	GATGAGTCCTGAGTAA**CTG**
M8 or M-CTT	AFLPMseI-8	GATGAGTCCTGAGTAA**CTT**
M9 or M-CGT	AFLPMseI-9	GATGAGTCCTGAGTAA**CGT**
M10 or M-CGG	AFLPMseI-10	GATGAGTCCTGAGTAA**CGG**
M11 or M-CGA	AFLPMseI-11	GATGAGTCCTGAGTAA**CGA**
M12 or M-CGC	AFLPMseI-12	GATGAGTCCTGAGTAA**CGC**
M13 or M-CCA	AFLPMseI-13	GATGAGTCCTGAGTAA**CCA**
M14 or M-CCC	AFLPMseI-14	GATGAGTCCTGAGTAA**CCC**
M15 or M-CCG	AFLPMseI-15	GATGAGTCCTGAGTAA**CCG**
M16 or M-CCT	AFLPMseI-16	GATGAGTCCTGAGTAA**CCT**
EcoR1-+1A	EcoRI pre-amp	GACTGCGTACCAATTC**A**
MseI-+1C	MseI pre-amp	GATGAGTCCTGAGTAA**C**
	EcoRI ADAPTER-F	CTCGTAGACTGCGTACC
	EcoRI ADAPTER-R	AATTGGTACGCAGTCTAC
	MseI ADAPTER-F	TACTCAGGACTCAT
	MseI ADAPTER-R	GACGATGAGTCCTGAG

Table 17. Approx. 62 primer combos out of the 255 screened (62/255 x 100 = 24%) were identified from archived gels to possess sufficient polymorphism to merit further analysis.

	M1-CAA	M2-CAC	M3-CAG	M4-CAT	M5-CTA	M6-CTC	M7-CTG	M8-CTT	M9-CGT	M10-CGG	M11-CGA	M12-CGC	M13-CCA	M14-CCC	M15-CCG	M16-CCT
E1 AAC									X			X				
E2 AAG									X	X		X				
E3 ACA									X	X	X				X	
E4 ACC				ND					X	X						
E5 ACG		X	X	X			X	X			X	X			X	
E6 ACT									X	X	X					
E7 AGC			X							X	X	X				
E8 AGG			X	X					X	X	X	X		X	X	
E9 AAA			X						X			X				
E10 AGA		X							X	X	X	X	X		X	
E11 AAT									X	X	X					X
E12 AGT									X	X	X		X			
E13 ATA									X	X						
E14 ATC																
E15 ATG							X		X	X				X	X	X
E16 ATT					X					X						

ND, Not determined.

Fig. 1A. One primer combination E5-M7 (E5= GACTGCGTACCAATTC**ACG** and M7= GATGAGTCCTGAGTAA**CTG**) **which appeared to clearly differentiate among all four parental genotypes.** From left to right lane 1=C02074; 2=C03058; 3=C03028; and 4=C04016. Gel run and archived as a *.tif file on Sept 9, 2005. Bands shown from top portion of gel range from about 800 to 200 bases.

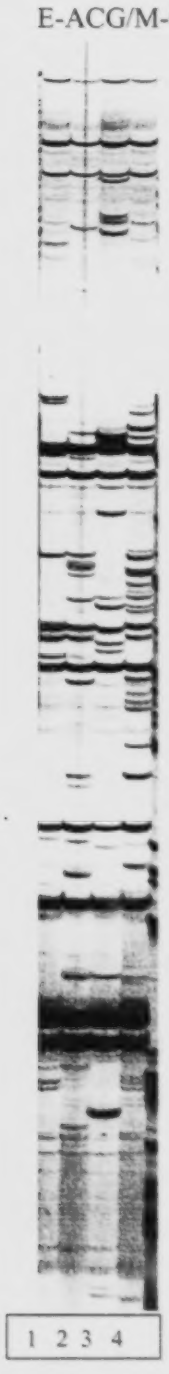

Table 18. 109 Oat specific SSR primer sets and their sequences.

Primer set [z]	Forward	5' to 3' sequence	Reverse	5' to 3' sequence
1	AM1-f	GGATCCTCCACGCTGTTGA	AM1-r	CTCATCCGTATGGGCTTTA
2	AM2-f	TGAATTCGTGGCATAGTCACAAGA	AM2-r	AAGGAGGGCATAGGGAGGTATTT
3	AM3-f	CTGGTCATCCTCGCCGTTCA	AM3-r	CATTTAGCCAGGTTGCCAGGTC
4	AM4-f	GGTAAGGTTTCGAAGAGCAAAG	AM4-r	GGGCTATATCCATCCCTCAC
5	AM5-f	TTGTCAGCGAAATAAGCAGAGA	AM5-r	GAATTCGTGACCAGCAACAG
6	AM6-f	AATGAAGAAACGGGTGAGGAAGTG	AM6-r	CCAGCCCAGTAGTTAGCCCATCT
7	AM7-f	GTGAGCGCCGAATACATA	AM7-r	TTGGCTAGCTGCTTGAAACT
8	AM8-f	CAAGGCATGGAAAGAAGTAAGAT	AM8-r	TCGAAGCAACAAATGGTCACAC
9	AM9-f	CAAAGCATTGGGCCCTTGT	AM9-r	GGCTTTGGGACCTCCTTTCC
10	AM10-f	AAAATCGGGGAAGGAAACC	AM10-r	GAAGGCAAAATACATGGAGTCAC
11	AM11-f	TCGTGGCAGAGAATCAAAGACA	AM11-r	TGGGTGGAGGCAAAAACAAAAC
12	AM12-f	TGCTGAAGTGAACAATCGC	AM12-r	CCTTCTCCAACAACTCTAC
13	AM13-f	CGGCGTGATTTGGGGAAGAAG	AM13-r	CTAGTAACGGCCGCCAGTGTGCTG
14	AM14-f	GTGGTGGGCACGGTATCA	AM14-r	TGGGTGGCGAAGCGAATC
15	AM15-f	GTGACCGATAACGATAACAAC	AM15-r	AAGCAAGACGCGAGAGTAGG
16	AM16-f	CGGGTGGCATCGACTATGA	AM16-r	TGACCAGGCTCTAACACA
17	AM17-f	CGAGATTTCGGTGTATGTGA	AM17-r	CCGGGAATTAACGGAGTC
18	AM18-f	CAATGTCGTCGGGTGAGTTT	AM18-r	TACGAGTGTGGCACGAGC
19	AM19-f	ATAGAACGGCATGATAACGAAATA	AM19-r	GCGCGACAACAGGATGCA
20	AM20-f	TGTCGATTTCTTTAGGGCAGCACT	AM20-r	TCGCGAGAAAGATGGAAAGGAGAG
21	AM21-f	ACGTTGGTCTCGGGTTGG	AM21-r	AAATCCTTGACTTCGCTCTGA
22	AM22-f	ATTGTATTTGTAGCCCCAGTTC	AM22-r	AAGAGCGACCCAGTTGTATG
23	AM23-f	TCTTTAAGGATTTGGGTGGAG	AM23-r	AATCTTCGAGGGTGAGTTTCT
24	AM24-f	GTTATTGATTTCCTGATGTAGAGA	AM24-r	AGAGCCAAGAAACGAACTG
25	AM25-f	AGCCTGGACATGTAATCTGGT	AM25-r	AGCCCTGGTCTTCTTCAACA
26	AM26-f	ATAAAGGGGGCATTGGATT	AM26-r	AACATATTGGGCATTCACAT
27	AM27-f	CAAAGGCCAAATGGTGAG	AM27-r	CCGCAAAGTCATATGGAGCAT
28	AM28-f	GACCTCTTGAGTAAGCAACG	AM28-r	TGGTCTTCCTATCCACAATG
29	AM29-f	TCCCGCAAAATCATCACGA	AM29-r	AAGGGAGCATTGGTTTTGTT
30	AM30-f	TGAAGATAGCCATGAGGAAC	AM30-r	GTGCAAATTGAGTTTCACG
31	AM31-f	GCAAAGGCCATATGGTGAGAA	AM31-r	CATAGGTTTGCCATTCGTGGT
32	AM32-f	AGTGAAGGCGATGGCGAA	AM32-r	GGATAATGCACCCGAGTTGC
33	AM33-f	GCAAAGGTTAAATGGTGAGA	AM33-r	GCCAACATATTGTGCATACA
34	AM34-f	GAGTAAGCAAAGGTCAAATG	AM34-r	GTTAGCACTTCCCACAAAATCA
35	AM35-f	CGTGACCTTTATATCACCACT	AM35-r	GTGGCTCGTGATATTGGCAC
36	AM36-f	CTTCCCGCAAAGTTATCAT	AM36-r	AGGGGCATTGGCTTTGTC
37	AM37-f	CTTCCACAAGGCAACGAGTC	AM37-r	GGTTAGCACTTCCCGCAAA
38	AM38-f	TGATGACCTCTTGAGTAAGCA	AM38-r	TGCCTTTCGTGGACTTACTA
39	AM39-f	TTGGGCCATGCCCTTGTT	AM39-r	GCCTTGGAGAGTAAATTCTC
40	AM40-f	CTCTGGGGGTGGTAGTTCCT	AM40-r	GAAAGACAGGCCTCCACAAAT
41	AM41-f	CCCAAAGGAAACAAGTCAATAG	AM41-r	TTCCCGCAAAGTCATCAT
42	AM42-f	GCTTCCCGCAAATCATCAT	AM42-r	GAGTAAGCAAAGGCCAAAAAGT
43	AM43-f	AGCCCCTACAAAGCCATCA	AM43-r	CAAGCAAAGGACGAACAATAG
44	AM44-f	CGTGGCCCCTTTTTCAGTG	AM44-r	AGGGGCATTGGCTTTGTCC
45	AM45-f	AGGGAAAAACAAAACGTGAGAGTA	AM45-r	ATGCAACAGATAGACAAGGGATTA
46	AM46-f	TTGGCAAGGCGAGGTCT	AM46-r	CGCCAAAAGGCTACAACATCACCG
47	AM47-f	GCACCGGTTAAAAAGGAGTCAG	AM47-r	TTTCTTCTTACCCACCCACCAC
48	AM48-f	ATTCGTGGCTCCTGTGC	AM48-r	GTGTACGTTAACTCCCCTCTAT
49	AM49-f	TAGAAAAAGGAAAGTTAGGGTTAG	AM49-r	TGAAATTGACTGTTATGTGGTTAC
50	AM50-f	CTTGAGCGCTAGATGGTTCC	AM50-r	CTCTGTTACTCAAGTGTTTCAATA
51	AM51-f	AATCGGACCTATGCAAGTTTCAG	AM51-r	AGTCGGACGCTCTATCATTCTCA
52	AM52-f	ATAGTGCCATGACCAATCTT	AM52-r	GTCTAGCCCACTCAAACACCA
53	AM53-f	TCGCCATTAATAAGAGGGAAGG	AM53-r	GCTGCTGTTGGGTGGTTAGTG
54	AM54-f	AAACCCGTGCAAGAAACCAA	AM54-r	TGCGGGAGGAGGGAAGAC

55	AM55-f	TATTTGCGGGCTGAAGTTTGTA	AM55-r	GGTCATTTGATATCTCCATTCTA
56	AM56-f	CGCGACGGCTTTGTGTT	AM56-r	CCGCGCCTCTTTGGTATT
57	AM57-f	TCACGCGATGGGCAGAA	AM57-r	CGCGCTTCCAAGGTATTATC
58	AM58-f	GTTTAGATGGGGGTGGCTTAG	AM58-r	TTTCTTGTTCTTTGGATTTTATTT
59	AM59-f	TCTGGGCTACGAAAATGTT	AM59-r	CCGGCGGAAATGGAGTG
60	AM60-f	GAAGCGCGTCAGTTGATG	AM60-r	AGCCCACGTTCACTCCAT
61	AM61-f	TCGGAGCCGGTATGGAAGC	AM61-r	GGTGGCAAGGGGTGTATGAG
62	AM81-f	ACGGGCTACCCCTGTTAGAA	AM81-r	GGGACACATGCAATCACCTA
63	AM82-f	CACAAGTTGGGGCACTATCC	AM82-r	GGAGGAAGACCACGAGAACA
64	AM83-f	CACTGCCATACATTCTGTCG	AM83-r	CCTCTACCGCAAAGGAAGAA
65	AM84-f	GATAACAACTTGGATGCAACTGA	AM84-r	CAGGTTGACAAGGGAACGAT
66	AM85-f	CACCAAGACGATTCGCTACA	AM85-r	CTTTTGCAAGACCTTCAAATCA
67	AM86-f	ACAACTCCTTGCGGGTCATA	AM86-r	AGTGCATGCGAATTTTTCAG
68	AM87-f	GAGCAAGCTCTGGATGGAAA	AM87-r	CCCGTTTATGTGGTTGTTAGC
69	AM88-f	ACATCGCCGAACATATTGCT	AM88-r	CATATCCTGACCGGGTCCT
70	AM89-f	GGCGGTTGGAGAGTGTCTT	AM89-r	AGGTGAAGGCGAGTGGAAG
71	AM90-f	GTCGGATGCGTATCTCTCGT	AM90-r	GAGAAGCTGCCGGTACCATA
72	AM91-f	GCGATTTACAACGACCTTATGA	AM91-r	CCAGTGCTTCTGATCTGGAAT
73	AM92-f	CCGCACTATCGGCTTGTATC	AM92-r	GTGGGAATCGAGGGTAGAGC
74	AM93-f	CCGACATTGCATATGCTGTTA	AM93-r	TTGATAACCAAAGGCAGATTATGA
75	AM94-f	TCTGGAAGTGGTAGTGGGTGT	AM94-r	AACCCATCCACCATAGGC
76	AM95-f	GGCAGGAAGTGGGTCAGATA	AM95-r	CTGAGAACTCGGCCTAGGAA
77	AM96-f	CCAAAAGGCCGATTGTGATA	AM96-r	AACCCTCTTTTGCGGTCAAT
78	AM97-f	TGGGTAGTCCTGGAGCTGAAGCG	AM97-r	GCCATACGACGAGCACCACAAAG
79	AM98-f	GATCTTGGCGTCGGGCGTTAG	AM98-r	AGTAACAACCGAGTGCGATGCTCC
80	AM99-f	GCAATCATTCCAACTTGTTATGACACA	AM99-r	GATAGTGGAAGCGGCATCAACATC
81	AM100-f	CGCTGTCCAATGTTCCACTCCTG	AM100-r	CAGTTGATAACCAAAAGGCTGATTGTG
82	AM101-f	CGCTTATCACCCACAGACCGAC	AM101-r	CACAATCTGCCTTTGGTTATCAACTG
83	AM102-f	TGGTCAGCAAGCATCACAAT	AM102-r	TGTGCATGCATCTGTGCTTA
84	AM103-f	CAACAACTTGGATGCAACAGA	AM103-r	CATCAACGTGAGGTTCTCCA
85	AM104-f	AACAATGATGGGGATGGTGT	AM104-r	GTCGTGAGCAAGTTGAACCA
86	AM105-f	GTCGCGGGTAGCTTAATGG	AM105-r	ACTGTGATCCAAGTCGTCCA
87	AM106-f	CAAGCATCTGCAGACTCACC	AM106-r	GGGAACCAGTTAGGCTCAAA
88	AM107-f	CCGTGGTATGAGTGCTAATGAA	AM107-r	TTTTCATGAGGTTGTCCTTGG
89	AM108-f	ATCCCAAGTACACCCCTTCC	AM108-r	GCACAATGGCATGACGTAAC
90	AM109-f	ACCCCTGTCAGAGGAACGTC	AM109-r	GGGACACATGCAAGAACCTA
91	AM110-f	TTCATCGCTGTGACCATGTG	AM110-r	TCCGTGAGTTCCCTCAGTTC
92	AM111-f	CAAGTGGGCGGAGTTAGGTA	AM111-r	TCTTCGGTGTGAGTTTCCAA
93	AM112-f	AGCGGTGTAGGGGAAAGAGT	AM112-r	TTCTTGGTTTAGATGGGAGGA
94	AM113-f	ATCAAAGATCGCCTCGAGTT	AM113-r	GGTCCAACATAGGCACAAGG
95	AM114-f	TTCGACAGTGAGTTATCCTTGC	AM114-r	CAATGCATGGCACAGTCAA
96	AM115-f	CGCAACTCTTCCTACTTTTTGTT	AM115-r	TGGCAAACTCCCTCGATTTA
97	AM116-f	TCGAAAATCAGAAGTTATACAACAAAA	AM116-r	TCAATCTCAAGAACCTGGTAAGCA
98	AM117-f	CACTACCCGCAAAGTCATCA	AM117-r	AGGACACATTTCCAGCAAGG
99	AM118-f	TCCATTGCATGACCTCTTGA	AM118-r	ACTTCCCGCAAAATCATCAC
100	AM119-f	GCATTGGCTTTGTCCCTAAA	AM119-r	GTTTTGCCATTCGTGGACTT
101	AM120-f	GCAAGCAAAGGACGAACAAT	AM120-r	TGGGAACCCAAATAGACCAA
102	AM121-f	GGAATTGGCTTTGTCTCCAA	AM121-r	TGGTCTTACTCGCCACAATG
103	AM122-f	TAGCTAAGGCCACCTTTCCA	AM122-r	TTAGCACTTCCCGCAAAATC
104	AM123-f	TAATTTCCTCCCTGACCGTG	AM123-r	CTCAGACCTGCGAACAAACA
105	AM124-f	TTTGAAGGATCAACTTGCCA	AM124-r	AGGGTTAGGCCATTTGGAAC
106	OAC26-U	CACCCTCATGCCAATTGGA	OAC26-L	ACGGGCGGCTCTACATGAT
107	OAC35-U	TGCATAGACCATTTGGCAACA	OAC35-L	TTGATTGTGTGTTCATGCGGT
108	OJ15U	ATCGCGCCGGTTCTCAA	AM47-r	TTTCTTCTTACCCACCCACCAC
109	AM18-f	CAATGTCGTCGGGTGAGTTT	OAC13L	GCTGGAATTCGGGCTTTTTT

[Z] Primer sets nos. 1 to 61 were taken from Li et al., (2000). Primer sets nos. 62-105 were taken from Pal et al., (2002). Primers AM22 and AM23 were replaced by primer sets nos 106 and 107 while only one primer

within primer sets nos 108 and 109 were replaced, OJ15U and OAC13L respectively (Mr. P. Eckstein and Dr. G. Scoles, personnel communication; *erratum unpublished*).

Table 19. Summary of oat SSR work in canaryseed using ten parental canaryseed lines.

Primer set	Forward primer	Revers primer	Touchdown anealing temperature (°C)	Band intensity	Tested with 10 parental lines[z] Polymorphism on 2.5% Agarose	3% metaphor
1	AM1-f	AM1-r	46-40	Good	None	None
2	AM2-f	AM2-r	No bands <300 bp	NA	NA	NA
3	AM3-f	AM3-r	46-40	G	None	None
4	AM4-f	AM4-r	46-40	G	None	None
5	AM5-f	AM5-r	46-40	G	None	ND
6	AM6-f	AM6-r	46-40	G	None	None
7	AM7-f	AM7-r	46-40	G	None	ND
8	AM8-f	AM8-r	46-40	G	None	ND
9	AM9-f	AM9-r	No bands <300 bp	NA	NA	NA
10	AM10-f	AM10-r	46-40	G	None	ND
11	AM11-f	AM11-r	46-40	G	None	ND
12	AM12-f	AM12-r	No bands <300 bp	NA	NA	NA
13	AM13-f	AM13-r	No bands <300 bp	NA	NA	NA
14	AM14-f	AM14-r	46-40	G	None	None
15	AM15-f	AM15-r	62-40	G	None	yes
16	AM16-f	AM16-r	46-40	G	None	ND
17	AM17-f	AM17-r	46-40	G	None	ND
18	AM18-f	AM18-r	46-40	G	ND	ND
19	AM19-f	AM19-r	46-40	G	ND	ND
20	AM20-f	AM20-r	46-40	G	ND	ND
21	AM21-f	AM21-r	46-40	G	None	ND
22	AM22-f	AM22-r	46-40	G	None	ND
23	AM23-f	AM23-r	46-40	G	None	None
24	AM24-f	AM24-r	46-40	G	ND	ND
25	AM25-f	AM25-r	46-40	G	None	None
26	AM26-f	AM26-r	No bands <300 bp	NA	NA	NA
27	AM27-f	AM27-r	62-40	G	None	ND
28	AM28-f	AM28-r	No bands <300 bp	NA	NA	NA
29	AM29-f	AM29-r	53-40	G	None	ND
30	AM30-f	AM30-r	46-40	WEAK	ND	ND
31	AM31-f	AM31-r	46-40	G	None	None
32	AM32-f	AM32-r	53-40	G	None	ND
33	AM33-f	AM33-r	53-40	G	None	None
34	AM34-f	AM34-r	46-40	G	None	ND
35	AM35-f	AM35-r	46-40	G	ND	ND
36	AM36-f	AM36-r	46-40	G	None	ND
37	AM37-f	AM37-r	46-40	G	ND	ND
38	AM38-f	AM38-r	46-40	G	None	ND
39	AM39-f	AM39-r	No bands <300 bp	NA	NA	NA
40	AM40-f	AM40-r	46-40	G	ND	ND
41	AM41-f	AM41-r	46-40	WEAK	ND	ND
42	AM42-f	AM42-r	46-40	G	None	None
43	AM43-f	AM43-r	46-60	WEAK	None	ND
44	AM44-f	AM44-r	46-40	G	None	ND
45	AM45-f	AM45-r	53-40	G	None	ND
46	AM46-f	AM46-r	62-40	G	None	ND
47	AM47-f	AM47-r	No bands <300 bp	NA	NA	NA
48	AM48-f	AM48-r	46-40	WEAK	ND	ND
49	AM49-f	AM49-r	46-40	G	None	None
50	AM50-f	AM50-r	46-40	G	ND	ND
51	AM51-f	AM51-r	46-40	G	None	ND
52	AM52-f	AM52-r	No bands <300 bp	NA	NA	NA
53	AM53-f	AM53-r	46-40	G	ND	ND
54	AM54-f	AM54-r	46-40	G	None	None
55	AM55-f	AM55-r	No bands <300 bp	NA	NA	NA
56	AM56-f	AM56-r	46-40	WEAK	ND	ND
57	AM57-f	AM57-r	46-40	G	None	None
58	AM58-f	AM58-r	No bands <300 bp	NA	NA	NA
59	AM59-f	AM59-r	46-40	G	ND	ND
60	AM60-f	AM60-r	46-40	G	None	ND
61	AM61-f	AM61-r	46-40	G	None	ND
62	AM81-f	AM81-r	46-40	G	None	None
63	AM82-f	AM82-r	53-40	G	None	ND
64	AM83-f	AM83-r	46-40	G	None	ND

65	AM84-f	AM84-r	46-40	WEAK	ND	ND
66	AM85-f	AM85-r	46-40	G	ND	ND
67	AM86-f	AM86-r	46-40	WEAK	ND	ND
68	AM87-f	AM87-r	No bands <300 bp	NA	NA	NA
69	AM88-f	AM88-r	46-40	G	ND	ND
70	AM89-f	AM89-r	46-40	G	None	ND
71	AM90-f	AM90-r	46-40	G	ND	ND
72	AM91-f	AM91-r	No bands <300 bp	NA	NA	NA
73	AM92-f	AM92-r	46-40	G	ND	ND
74	AM93-f	AM93-r	No bands <300 bp	NA	NA	NA
75	AM94-f	AM94-r	53-40	G	None	ND
76	AM95-f	AM95-r	62-40	G	None	ND
77	AM96-f	AM96-r	No bands <300 bp	NA	NA	NA
78	AM97-f	AM97-r	46-40	G	None	ND
79	AM98-f	8-r	46-40	G	None	ND
80	AM99-f	9-r	46-40	G	None	None
81	AM100-f	AM100-r	46-40	G	None	ND
82	AM101-f	AM101-r	No bands <300 bp	NA	NA	NA
83	AM102-f	AM102-r	46-40	G	None	None
84	AM103-f	AM103-r	62-40	G	None	None
85	AM104-f	AM104-r	53-40	WEAK	None	ND
86	AM105-f	AM105-r	62-40	G	None	None
87	AM106-f	AM106-r	62-40	G	None	yes
88	AM107-f	AM107-r	No bands <300 bp	NA	NA	NA
89	AM108-f	AM108-r	46-40	G	None	ND
90	AM109-f	AM109-r	62-40	G	None	yes
91	AM110-f	AM110-r	46-40	G	ND	ND
92	AM111-f	AM111-r	46-40	G	None	ND
93	AM112-f	AM112-r	46-40	WEAK	ND	ND
94	AM113-f	AM113-r	46-40	G	ND	ND
95	AM114-f	AM114-r	46-40	G	None	ND
96	AM115-f	AM115-r	No bands <300 bp	NA	NA	NA
97	AM116-f	AM116-r	No bands <300 bp	NA	NA	NA
98	AM117-f	AM117-r	46-40	G	ND	ND
99	AM118-f	AM118-r	46-40	G	None	ND
100	AM119-f	AM119-r	No bands <300 bp	NA	NA	NA
101	AM120-f	AM120-r	62-40	G	None	None
102	AM121-f	AM121-r	46-40	G	ND	ND
103	AM122-f	AM122-r	46-40	G	ND	ND
104	AM123-f	AM123-r	No bands <300 bp	NA	NA	NA
105	AM124-f	AM124-r	46-40	G	None	ND
106	OAC26-U	OAC26-L	46-40	G	ND	ND
107	OAC35-U	OAC35-L	46-40	G	ND	ND
108	OJ15U	AM47-r	62-40	G	None	None
109	AM18-f	OAJC13L	46-40	G	ND	ND

[z] ND= Not determined; NA = Not applicable.